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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/023,597

DATE: 09/17/2002

TIME: 12:40:44

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3 <110> APPLICANT: Padigaru, Muralidhara
4 Kekuda, Ramesh
5 Li, Li
6 Ballinger, Robert A.
7 Casman, Stacie J.
8 Spytek, Kimberly A.
9 Baumgartner, Jason C.
10 Burgess, Catherine E.
12 <120> TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
14 <130> FILE REFERENCE: 21402-224AD
16 <140> CURRENT APPLICATION NUMBER: 10/023,597
17 <141> CURRENT FILING DATE: 2001-12-18
19 <150> PRIOR APPLICATION NUMBER: 60/256,635
20 <151> PRIOR FILING DATE: 2000-12-18
22 <150> PRIOR APPLICATION NUMBER: 60/259,743
23 <151> PRIOR FILING DATE: 2001-01-04
25 <150> PRIOR APPLICATION NUMBER: 60/299,327
26 <151> PRIOR FILING DATE: 2001-06-19
28 <150> PRIOR APPLICATION NUMBER: 60/261,498
29 <151> PRIOR FILING DATE: 2001-01-12
31 <150> PRIOR APPLICATION NUMBER: 60/263,689
32 <151> PRIOR FILING DATE: 2001-01-24
34 <150> PRIOR APPLICATION NUMBER: 60/267,464
35 <151> PRIOR FILING DATE: 2001-02-08
37 <150> PRIOR APPLICATION NUMBER: 60/271,021
38 <151> PRIOR FILING DATE: 2001-02-22
40 <150> PRIOR APPLICATION NUMBER: 60/275,946
41 <151> PRIOR FILING DATE: 2001-03-14
43 <150> PRIOR APPLICATION NUMBER: 60/278,150
44 <151> PRIOR FILING DATE: 2001-03-23
46 <150> PRIOR APPLICATION NUMBER: 60/285,718
47 <151> PRIOR FILING DATE: 2001-04-03
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55 <150> PRIOR APPLICATION NUMBER: 60/260,718
56 <151> PRIOR FILING DATE: 2001-01-10
58 <150> PRIOR APPLICATION NUMBER: 60/284,591
59 <151> PRIOR FILING DATE: 2001-04-18
61 <160> NUMBER OF SEQ ID NOS: 128
63 <170> SOFTWARE: PatentIn Ver. 2.1
65 <210> SEQ ID NO: 1

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66 <211> LENGTH: 967

67 <212> TYPE: DNA

68 <213> ORGANISM: Homo sapiens

70 <400> SEQUENCE: 1

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73 tgctaacatc atcattgtga ctatcatctg cattgaccat catctccaca ctcccatgta 180
74 tttcttccta agcatgctgg ctagttcaga gacggtgtac acactgggtca ttgtgccacg 240
75 aatgcttttg agcctcattt ttcataacca acctatctcc ttggcaggct gtgctacaca 300
76 aatgttcttt ttgttatct tggccactaa taattgcttc ctgcttactg caatggggta 360
77 tgaccgctat gtggccatct gcagaccctt gagatacact gtcacatga gcaagggact 420
78 atgtgcccag ctggtgtgtg ggtccttttg cattggtctg actatggcag ttctccatgt 480
79 gacagccatg ttcaatttgc cgttctgtgg cacagtggta gaccacttct tttgtgacat 540
80 ttaccagctc atgaaacttt cttgcattga taccactatc aatgagataa taaattatgg 600
81 tgtaagttca tttgtgattt ttgtgcccat aggcctgata tttatctcct atgtccttgt 660
82 catctcttcc atccttcaaa ttgcctcagc tgagggcccg aagaagacct ttgccacctg 720
83 tgtctcccac ctactgttg ttattgtcca ctgtggctgt gcctccattg cctacctcaa 780
84 gccgaagtca gaaagttcaa tagaaaaaga ccttgttctc tcagtgaagt acaccatcat 840
85 cactcccttg ctgaaccctg ttgtttacag tctgagaaac aaggaggtaa aggatgcctt 900
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87 tagccca
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92 <212> TYPE: PRT

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95 <400> SEQUENCE: 2

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100      20             25             30
102 Thr Val Tyr Ile Leu Thr Leu Val Ala Asn Ile Ile Ile Val Thr Ile
103      35             40             45
105 Ile Cys Ile Asp His His Leu His Thr Pro Met Tyr Phe Phe Leu Ser
106      50             55             60
108 Met Leu Ala Ser Ser Glu Thr Val Tyr Thr Leu Val Ile Val Pro Arg
109      65             70             75             80
111 Met Leu Leu Ser Leu Ile Phe His Asn Gln Pro Ile Ser Leu Ala Gly
112      85             90             95
114 Cys Ala Thr Gln Met Phe Phe Phe Val Ile Leu Ala Thr Asn Asn Cys
115      100            105            110
117 Phe Leu Leu Thr Ala Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys Arg
118      115            120            125
120 Pro Leu Arg Tyr Thr Val Ile Met Ser Lys Gly Leu Cys Ala Gln Leu
121      130            135            140
123 Val Cys Gly Ser Phe Gly Ile Gly Leu Thr Met Ala Val Leu His Val
124      145            150            155            160
126 Thr Ala Met Phe Asn Leu Pro Phe Cys Gly Thr Val Val Asp His Phe
127      165            170            175
129 Phe Cys Asp Ile Tyr Pro Val Met Lys Leu Ser Cys Ile Asp Thr Thr

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132 Ile Asn Glu Ile Ile Asn Tyr Gly Val Ser Ser Phe Val Ile Phe Val
133          195          200          205
135 Pro Ile Gly Leu Ile Phe Ile Ser Tyr Val Leu Val Ile Ser Ser Ile
136          210          215          220
138 Leu Gln Ile Ala Ser Ala Glu Gly Arg Lys Lys Thr Phe Ala Thr Cys
139 225          230          235          240
141 Val Ser His Leu Thr Val Val Ile Val His Cys Gly Cys Ala Ser Ile
142          245          250          255
144 Ala Tyr Leu Lys Pro Lys Ser Glu Ser Ser Ile Glu Lys Asp Leu Val
145          260          265          270
147 Leu Ser Val Thr Tyr Thr Ile Ile Thr Pro Leu Leu Asn Pro Val Val
148          275          280          285
150 Tyr Ser Leu Arg Asn Lys Glu Val Lys Asp Ala Leu Cys Arg Val Val
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165 cattgctggg caacctttctc atcatggcca caatctggat tgaacacaga ctccacacac 180
166 ccatgtacct cttcttgtgc accctctccg tctctgagat tctgttcaact gttgccatca 240
167 cccctcgcat gctggctgat ctgctttcca cccatcattc catcaccttt gtggcttggtg 300
168 ccaaccagat gttctttctcc ttcattgtttg gcttcaactca ctcttctcctt ctcttggtca 360
169 tgggctatga tcgctatgtg gccatctgcc acccactgcg ttacaatgtg ctcatgagcc 420
170 cccgtgactg tgcccatctt gtggcctgta cctgggctgg tggctcagtc atggggatga 480
171 tggtgacaac gatagttttc cacctcactt tctgtgggtc taatgtgatc caccattttt 540
172 tctgtcatgt gctttccctc ttgaagtgtg cctgtgaaaa caagacatca tctgtcatca 600
173 tgggtgtgat gctggtgtgt gtcacagccc tgataggctg ttatttcctc atcatcctct 660
174 cctatgtctt cattgtggct gccatcttga ggattccctc tgccgaaggc cggcacaaga 720
175 cattttctac gtgtgtatcc cacctcactg tgggtggtcac gcactatagt tttgcctcct 780
176 ttatctacct caagcccaag ggccctcatt ctatgtacag tgacgccttg atggccacca 840
177 cctatactgt cttcaccccc ttcttagcc caatcatttt cagcctaagg aacaaggagc 900
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179 ca
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189 1 5 10 15
191 Phe Ser Ala Phe Pro Gln His Leu Leu Pro Ile Leu Phe Leu Leu Tyr
192 20 25 30
194 Leu Leu Met Phe Leu Phe Thr Leu Leu Gly Asn Leu Leu Ile Met Ala

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195          35          40          45
197 Thr Ile Trp Ile Glu His Arg Leu His Thr Pro Met Tyr Leu Phe Leu
198          50          55          60
200 Cys Thr Leu Ser Val Ser Glu Ile Leu Phe Thr Val Ala Ile Thr Pro
201 65          70          75          80
203 Arg Met Leu Ala Asp Leu Leu Ser Thr His His Ser Ile Thr Phe Val
204          85          90          95
206 Ala Cys Ala Asn Gln Met Phe Phe Ser Phe Met Phe Gly Phe Thr His
207          100          105          110
209 Ser Phe Leu Leu Leu Val Met Gly Tyr Asp Arg Tyr Val Ala Ile Cys
210          115          120          125
212 His Pro Leu Arg Tyr Asn Val Leu Met Ser Pro Arg Asp Cys Ala His
213          130          135          140
215 Leu Val Ala Cys Thr Trp Ala Gly Gly Ser Val Met Gly Met Met Val
216 145          150          155          160
218 Thr Thr Ile Val Phe His Leu Thr Phe Cys Gly Ser Asn Val Ile His
219          165          170          175
221 His Phe Phe Cys His Val Leu Ser Leu Leu Lys Leu Ala Cys Glu Asn
222          180          185          190
224 Lys Thr Ser Ser Val Ile Met Gly Val Met Leu Val Cys Val Thr Ala
225          195          200          205
227 Leu Ile Gly Cys Leu Phe Leu Ile Ile Leu Ser Tyr Val Phe Ile Val
228          210          215          220
230 Ala Ala Ile Leu Arg Ile Pro Ser Ala Glu Gly Arg His Lys Thr Phe
231 225          230          235          240
233 Ser Thr Cys Val Ser His Leu Thr Val Val Val Thr His Tyr Ser Phe
234          245          250          255
236 Ala Ser Phe Ile Tyr Leu Lys Pro Lys Gly Leu His Ser Met Tyr Ser
237          260          265          270
239 Asp Ala Leu Met Ala Thr Thr Tyr Thr Val Phe Thr Pro Phe Leu Ser
240          275          280          285
242 Pro Ile Ile Phe Ser Leu Arg Asn Lys Glu Leu Lys Asn Ala Ile Asn
243          290          295          300
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257 tctgtgggaa tgtcctcctc atcttctcca tctacatgga ccctcacctt cacaccccca 180
258 tgtacttctt cctcagccag ctctccctca tggacctcat gttggtctgt accaatgtgc 240
259 caaagatggc agccaacttc ctgtctggca ggaagtccat ctcttttgtg ggctgtggca 300
260 tacaaatttg cctctttgtc tgtcttgagg gatctgaggg gctcttgctg ggactcatgg 360
261 cttatgaccg ctatgtggcc attagccacc cacttcacta tcccatcctc atgaatcaga 420
262 ggggtctgtc ccagattact gggagctcct gggcctttgg gataatcgat ggcttgatcc 480
263 agatggtggt agtaatgaat ttcccctact gtggcttgag gaaggtgaac catttcttct 540

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265 tatttgcttg ctgtgtcttc atgcttctct tccattctc catcatcgtg gcctcctatg 660
266 ctcacattct agggactgtg ctgcaaatgc actctgctca ggccctggaaa aaggccctgg 720
267 ccacctgctc ctcccacctg acagctgtca ccctcttcta tggggcagcc atgttcatct 780
268 acctgaggcc taggcactac cgggccccca gccatgacaa ggtggcctct atcttctaca 840
269 cggtccttac tcccatgctc aaccccctca ttacagctt gaggaacagg gaggtgatgg 900
270 gggcactgag gaaggggctg gaccgctgca ggatcggcag ccagcactga acccagggca 960
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284 20 25 30
286 Met Ala Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Leu Ile Phe
287 35 40 45
289 Leu Ile Tyr Met Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu
290 50 55 60
292 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Thr Asn Val Pro
293 65 70 75 80
295 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
296 85 90 95
298 Gly Cys Gly Ile Gln Ile Gly Leu Phe Val Cys Leu Val Gly Ser Glu
299 100 105 110
301 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
302 115 120 125
304 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
305 130 135 140
307 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Leu Ile Gln
308 145 150 155 160
310 Met Val Val Val Met Asn Phe Pro Tyr Cys Gly Leu Arg Lys Val Asn
311 165 170 175
313 His Phe Phe Cys Glu Met Leu Ser Leu Leu Lys Leu Ala Cys Val Asp
314 180 185 190
316 Thr Ser Leu Phe Glu Lys Val Ile Phe Ala Cys Cys Val Phe Met Leu
317 195 200 205
319 Leu Phe Pro Phe Ser Ile Ile Val Ala Ser Tyr Ala His Ile Leu Gly
320 210 215 220
322 Thr Val Leu Gln Met His Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
323 225 230 235 240
325 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
326 245 250 255
328 Met Phe Ile Tyr Leu Arg Pro Arg His Tyr Arg Ala Pro Ser His Asp
329 260 265 270
331 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
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